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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/727,084DATE: 04/11/97
TIME: 14:08:13

INPUT SET: S16960.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Pulst, Stefan M.

(ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
ATAXIA-2 AND PRODUCTS RELATED THERETO

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pretty, Schroeder & Poplawski

(B) STREET: 444 South Flower Street, Suite 2000

(C) CITY: Los Angeles

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 90071

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" diskette

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/727,084

(B) FILING DATE: October 8, 1996

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Viviana Amzel, Ph. D.

(B) REGISTRATION NUMBER: 30930

(C) REFERENCE/DOCKET NUMBER: P07 37217

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 213-622-7700

(B) TELEFAX: 213-489-4210

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

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47 (D) TOPOLOGY: both

48

49 (ii) MOLECULE TYPE: DNA (genomic)

50

51

52

53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

54

55 TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGGTC 60

56

57 TCGGCGGGCC TCCCCGCCCC TTCGTGCTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC 120

58

59 CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCC TCGTCCCCG CCGCGTTCCG 180

60

61 GCGTCTCCTT GGCGCGCCCC GCTCCCGGCT GTCCCCGCC GGCGTGCGAG CCGGTGTATG 240

62

63 GGCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC 300

64

65 AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA 360

66

67 AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT 420

68

69 CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG 480

70

71 GGAGGCCCCG CCTGGGCAGG TGGGTGTCGG CACCCC 516

72

73 (2) INFORMATION FOR SEQ ID NO:2:

74

75 (i) SEQUENCE CHARACTERISTICS:

76

77 (A) LENGTH: 4481 base pairs

78

79 (B) TYPE: nucleic acid

80

81 (C) STRANDEDNESS: both

82

83 (D) TOPOLOGY: both

84

85 (ii) MOLECULE TYPE: cDNA

86

87

88

89 (ix) FEATURE:

90

91 (A) NAME/KEY: CDS

92

93 (B) LOCATION: 163..4101

94

95

96 CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG 174

97

98

99 Met Arg Ser Ala 1
GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC 222

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| | | |
|-----|---|-----|
| 100 | Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe | |
| 101 | 5 10 15 20 | |
| 102 | | |
| 103 | GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG | 270 |
| 104 | Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg | |
| 105 | 25 30 35 | |
| 106 | | |
| 107 | CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC | 318 |
| 108 | Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser | |
| 109 | 40 45 50 | |
| 110 | | |
| 111 | GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC | 366 |
| 112 | Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser | |
| 113 | 55 60 65 | |
| 114 | | |
| 115 | TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC | 414 |
| 116 | Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly | |
| 117 | 70 75 80 | |
| 118 | | |
| 119 | GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT | 462 |
| 120 | Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro | |
| 121 | 85 90 95 100 | |
| 122 | | |
| 123 | CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC | 510 |
| 124 | Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala | |
| 125 | 105 110 115 | |
| 126 | | |
| 127 | CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC | 558 |
| 128 | Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser | |
| 129 | 120 125 130 | |
| 130 | | |
| 131 | CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC | 606 |
| 132 | Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro | |
| 133 | 135 140 145 | |
| 134 | | |
| 135 | CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG | 654 |
| 136 | Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys | |
| 137 | 150 155 160 | |
| 138 | | |
| 139 | CCC CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG | 702 |
| 140 | Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln | |
| 141 | 165 170 175 180 | |
| 142 | | |
| 143 | CAG CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC | 750 |
| 144 | Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg | |
| 145 | 185 190 195 | |
| 146 | | |
| 147 | AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG | 798 |
| 148 | Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser | |
| 149 | 200 205 210 | |
| 150 | | |
| 151 | CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG | 846 |
| 152 | Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr Ala Pro Ser Ser | |

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| | 215 | 220 | 225 | |
|-----|---|-----|-----|------|
| 153 | | | | |
| 154 | | | | |
| 155 | GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT | | | 894 |
| 156 | Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly | | | |
| 157 | 230 | 235 | 240 | |
| 158 | | | | |
| 159 | CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA | | | 942 |
| 160 | Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly | | | |
| 161 | 245 | 250 | 255 | 260 |
| 162 | | | | |
| 163 | ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC | | | 990 |
| 164 | Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly | | | |
| 165 | 265 | 270 | 275 | |
| 166 | | | | |
| 167 | TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT | | | 1038 |
| 168 | Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val | | | |
| 169 | 280 | 285 | 290 | |
| 170 | | | | |
| 171 | TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT | | | 1086 |
| 172 | Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His | | | |
| 173 | 295 | 300 | 305 | |
| 174 | | | | |
| 175 | GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG | | | 1134 |
| 176 | Glu Lys Ser Thr Glu Ser Ser Gly Pro Lys Arg Glu Glu Ile Met | | | |
| 177 | 310 | 315 | 320 | |
| 178 | | | | |
| 179 | GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA | | | 1182 |
| 180 | Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys | | | |
| 181 | 325 | 330 | 335 | 340 |
| 182 | | | | |
| 183 | GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT | | | 1230 |
| 184 | Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala | | | |
| 185 | 345 | 350 | 355 | |
| 186 | | | | |
| 187 | ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC | | | 1278 |
| 188 | Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro | | | |
| 189 | 360 | 365 | 370 | |
| 190 | | | | |
| 191 | TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA | | | 1326 |
| 192 | Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu | | | |
| 193 | 375 | 380 | 385 | |
| 194 | | | | |
| 195 | AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT | | | 1374 |
| 196 | Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn | | | |
| 197 | 390 | 395 | 400 | |
| 198 | | | | |
| 199 | GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG | | | 1422 |
| 200 | Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser | | | |
| 201 | 405 | 410 | 415 | 420 |
| 202 | | | | |
| 203 | TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG | | | 1470 |
| 204 | Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg | | | |
| 205 | 425 | 430 | 435 | |

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SEQUENCE VERIFICATION REPORT
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Original Text